

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 7/16/04
 Art Unit: 1635 Phone Number: 202-0765 Serial Number: 70/610,568
 Mail Box and Bldg/Room Location: 2C03 Results Format Preferred (circle): PAPER DISK E-MAIL

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Novel Human Protein
 Inventors (please provide full names): Ramstetter et al.

Earliest Priority Filing Date: 12/7/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 5/
 EXACT match needed. [800 NT] size limit
 (No interference search please.)

Please Search Seq ID No 1.
 size.
 Please limit to betw 10-50 NT.

Save over length if necessary.

No interference please.

80%
 cutoff Thanks.

STAFF USE ONLY

Searcher	Type of Search	Vendors and cost where applicable
Searcher: <u>D. Schreiber</u>	NA Sequence (#) <u>12</u>	STN
Searcher Phone #: <u>272-2526</u>	AA Sequence (#)	Dialog
Searcher Location: <u>Rosen Bldg</u>	Structure (#)	Questel/Orbit
Date Searcher Picked Up:	Bibliographic	Dr. Link
Date Completed: <u>7/26</u>	Litigation	Lexis/Nexis
Searcher Prep & Review Time: <u>15</u>	Fulltext	Sequence Systems <u>CompuGen</u>
Clerical Prep Time:	Patent Family	WWW/Internet
Online Time: <u>101</u>	Other	Other (specify)

SEARCH REQUEST FORM

Scientific and Technical Information Center

Requester's Full Name: JANE ZARA Examiner #: 77512 Date: 7/16/04
 Art Unit: 1635 Phone Number: 202-0765 Serial Number: 701010568
 Mail Box and Bldg/Room Location: 2C03 Results Format Preferred (circle): PAPER DISK E-MAIL
2018

If more than one search is submitted, please prioritize searches in order of need.

Please provide a detailed statement of the search topic, and describe as specifically as possible the subject matter to be searched. Include the elected species or structures, keywords, synonyms, acronyms, and registry numbers, and combine with the concept or utility of the invention. Define any terms that may have a special meaning. Give examples or relevant citations, authors, etc, if known. Please attach a copy of the cover sheet, pertinent claims, and abstract.

Title of Invention: Novel Human Protein

Inventors (please provide full names): _____

Ranestler et al.

Earliest Priority Filing Date: 12/7/01

For Sequence Searches Only Please include all pertinent information (parent, child, divisional, or issued patent numbers) along with the appropriate serial number.

Please Search Seq ID No: 5/
 EXACT match needed. [100 NT] size limit
 (No interference search please.)

Please Search Seq ID No 1.
 size.
 Please limit to betw 10-50 NT.

Save over length if necessary.

No interference please.

Thanks.

STAFF USE ONLY

Type of Search

Vendors and cost where applicable

Searcher: _____	NA Sequence (#) _____	STN _____
Searcher Phone #: _____	AA Sequence (#) _____	Dialog _____
Searcher Location: _____	Structure (#) _____	Questel/Orbit _____
Date Searcher Picked Up: _____	Bibliographic _____	Dr. Link _____
Date Completed: _____	Litigation _____	Lexis/Nexis _____
Searcher Prep & Review Time: _____	Fulltext _____	Sequence Systems _____
Clerical Prep Time: _____	Patent Family _____	WWW/Internet _____
Online Time: _____	Other _____	Other (specify) _____

GenCore version 5.1.6
Copyright (c) 1993 - 2004 CompuGen Ltd.

OM nucleic - nucleic search, using sw model

Run on: July 26, 2004, 09:15:49 ; Search time 1 Seconds
(without alignments)
5.092 Million cell updates/sec

Title: US-10-010-568-1
Perfect score: 1081
Sequence: 1 catattgccaactgaactc.....ccttgaattatttcattac 1081

Scoring table: IDENTITY_NUC
Gapop 10.0 , Gapext 0.5

Searched: 125 seqs, 2355 residues

Total number of hits satisfying chosen parameters: 250

Minimum DB seq length: 10
Maximum DB seq length: 50

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 129 summaries

Database : rge1.seq.*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	Query Match	Length	ID	Description
1	33	3.1	33	1	AX464563
2	33	3.1	33	1	AX464563
3	30	2.8	30	1	AX464564
4	30	2.8	30	1	AX464564
5	27.8	2.6	32	1	BD187509
6	27.8	2.6	32	1	BD171273
7	27	2.5	32	1	BD184763
8	27	2.5	32	1	BD171272
9	26	2.4	26	1	AX662013
10	26	2.4	26	1	AX662013
11	25.4	2.3	27	1	AX593363
12	25	2.3	25	1	AX482511
13	25	2.3	25	1	AX482512
14	25	2.3	25	1	AX482513
15	25	2.3	25	1	AX482514
16	25	2.3	25	1	AX662016
17	25	2.3	30	1	AX148227
18	24	2.2	24	1	AX148227
19	23	2.1	23	1	AX148226
20	23	2.1	23	1	AX148228
21	23	2.1	23	1	AX148229
22	22	2.0	22	1	AX458269
23	22	2.0	22	1	AX662012
24	22	2.0	22	1	AX662014
25	22	2.0	22	1	AX662017
26	22	2.0	22	1	AX675932
27	22	2.0	22	1	AX675934
28	21	1.9	25	1	AX147876
29	21	1.9	25	1	AX521925
30	20	1.9	20	1	AX458270
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37	19.4	1.8	21	1	AX521949
38	19.4	1.8	21	1	AX521978
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40	19	1.8	19	1	AX147898
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42	19	1.8	19	1	AX521923
43	19	1.8	19	1	AX521947
44	19	1.8	19	1	AX521976
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48	14.8	1.4	18	1	AR151366
49	14.8	1.4	18	1	AR295560
50	14.4	1.3	17	1	AR329420
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52	14.4	1.3	17	1	AX732335
53	14.4	1.3	18	1	AR131571
54	14.4	1.3	18	1	AR199505
55	14.4	1.3	18	1	AR200976
56	14.4	1.3	18	1	AX403678
57	14.4	1.3	18	1	AX147927
58	14.4	1.3	18	1	BD084989
59	14	1.3	17	1	AX759618
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87	13	1.2	15	1	BD208445
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89	12.8	1.2	16	1	AR028861
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93	12.6	1.2	22	1	AX458269
94	12.4	1.1	14	1	AR374278
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98	12.4	1.1	15	1	AR055975
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ACCESSION:BD201054	
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112 12.4 1.1 15 1 AX742794
113 12.4 1.1 15 1 BD184647
114 12.4 1.1 15 1 ACCESSION:BD208299
115 12.4 1.1 32 1 BD171272
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117 12 1.1 12 1 A47643
118 12 1.1 12 1 AR02979
119 12 1.1 12 1 AR027861
120 12 1.1 14 1 A12786
121 12 1.1 14 1 AR403521
122 12 1.1 14 1 BD069021
123 12 1.1 15 1 A83397
124 12 1.1 15 1 I39114
125 12 1.1 15 1 AR180550
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127 12 1.1 15 1 ACCESSION:AX635361
128 12 1.1 15 1 BD083622
129 12 1.1 15 1 BD208446

ALIGNMENTS

RESULT 1
AX464563
LOCUS AX464563 33 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 3 from Patent EP1219638.
ACCESSION AX464563
VERSION AX464563.1 GI:21899358
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fidoock,M.D.
TITLE G-protein coupled receptors having homology to the p2y
JOURNAL purinoreceptor 1 (p2y1)
Patent: EP 1219638-A 3 03-JUL-2002;
Pfizer Limited (GB) ; Pfizer Inc. (US)
FEATURES
source
1. .33
/organism="Homo sapiens"
/mol_type="unassigned DNA"
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Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 51 ACCATGAATGAGCCACTAGACTATTAGCAAAAT 83
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Db 1 ACCATGAATGAGCCACTAGACTATTAGCAAAAT 33

RESULT 2
BD187508
LOCUS BD187508 33 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Polypeptide.
ACCESSION BD187508
VERSION BD187508.1 GI:32997247
KEYWORDS JP 2003024081-A/2.
SOURCE Homo sapiens (human)
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fidoock,M.D.

Query Match 3.1%; Score 33; DB 1; Length 33;
Best Local Similarity 100.0%; Pred. No. 1.8;
Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

TITLE Novel Polypeptide
JOURNAL Patent: JP 2003024081-A 2 28-JAN-2003;
Pfizer Ltd (EP/GB only),Pfizer Inc (US JP EP except GB)
COMMENT OS Homo sapiens
PN JP 2003024081-A/2
PD 28-JAN-2003
PF 17-DEC-2001 JP 2001382712
PR 18-DEC-2000 GB 0030854.4,04-MAY-2001 GB 0111031.1 PI
mark david fidoock
CC
FH Key Location/Qualifiers.
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/organism="Homo sapiens"
/mol_type="genomic DNA"
/db_xref="taxon:9606"

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Matches 33; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

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Db 1 ACCATGAATGAGCCACTAGACTATTAGCAAAAT 33

RESULT 3
AX464564/c
LOCUS AX464564 30 bp DNA linear PAT 16-JUL-2002
DEFINITION Sequence 4 from Patent EP1219638.
ACCESSION AX464564
VERSION AX464564.1 GI:21899359
KEYWORDS Homo sapiens (human)
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fidoock,M.D.
TITLE G-protein coupled receptors having homology to the p2y
JOURNAL purinoreceptor 1 (p2y1)
Patent: EP 1219638-A 4 03-JUL-2002;
Pfizer Limited (GB) ; Pfizer Inc. (US)
FEATURES
source
1. .30
/organism="Homo sapiens"
/mol_type="unassigned DNA"
/db_xref="taxon:9606"

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Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 AAGAAATTTAGTTACTCAACACCCCTTGA 1067
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RESULT 4
BD187509/c
LOCUS BD187509 30 bp DNA linear PAT 17-JUL-2003
DEFINITION Novel Polypeptide.
ACCESSION BD187509
VERSION BD187509.1 GI:32997248
KEYWORDS JP 2003024081-A/3.
SOURCE Homo sapiens
ORGANISM Homo sapiens
REFERENCE 1
AUTHORS Fidoock,M.D.

Query Match 2.8%; Score 30; DB 1; Length 30;
Best Local Similarity 100.0%; Pred. No. 3.3;
Matches 30; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 1038 AAGAAATTTAGTTACTCAACACCCCTTGA 1067
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Db 30 AAGAAATTTAGTTACTCAACACCCCTTGA 1

INFORMATION FOR SEQ ID NO: 16;

SEQUENCE CHARACTERISTICS:

LENGTH: 15
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 MOLECULE TYPE: synthetic
 PUBLICATION INFORMATION:
 RELEVANT RESIDUES IN SEQ ID NO: 16: FROM 1 TO 15
 : -09-270-455-16

Query Match 1.1%; Score 12.4; DB 1; Length 15;
 Best Local Similarity 92.9%; Pred. No. 17;
 Matches 13; Conservative 0; Mismatches 1; Indels 0; Gaps 0;

1064 TTGAATATTCAT 1077
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 1 TTGAATATTCAT 14

SULT 33

-07-936-163-9/c
 Sequence 9, Application US/07936163
 Patent No. 5743477

GENERAL INFORMATION:
 APPLICANT: WALSH, TERENCE A
 APPLICANT: MERLO, DONALD J
 APPLICANT: HOUTCHENS, ROBERT A
 APPLICANT: STRICKLAND, JAMES A
 APPLICANT: ORR, GREGORY L
 TITLE OF INVENTION: INSECTICIDAL PROTEINS AND METHOD FOR
 TITLE OF INVENTION: PLANT PROTECTION
 NUMBER OF SEQUENCES: 49
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: THOMAS D. ZINDRICK
 STREET: 9002 PURDUE ROAD
 CITY: INDIANAPOLIS
 STATE: IN
 COUNTRY: US
 ZIP: 46268-1189

COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/07/936,163
 FILING DATE: 27-AUG-1992
 CLASSIFICATION: 514
 ATTORNEY/AGENT INFORMATION:
 NAME: ZINDRICK, THOMAS D
 REGISTRATION NUMBER: 32,185
 REFERENCE/DOCKET NUMBER: C-38,424A
 TELEPHONE: (517) 636-1869

INFORMATION FOR SEQ ID NO: 9:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 base pairs
 TYPE: nucleic acid
 STRANDEDNESS: single
 TOPOLOGY: linear
 07-936-163-9

Query Match 1.1%; Score 12; DB 1; Length 12;
 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

282 TGCACAGATCTG 293
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 12 TGCACAGATCTG 1

ULT 34

US-08-494-301A-3/c
 Sequence 3, Application US/08494301A
 Patent No. 5856461

GENERAL INFORMATION:
 APPLICANT: Colote, Soudhir
 APPLICANT: Pirotzky, Eduardo
 TITLE OF INVENTION: Oligonucleotides to Inhibit the
 TITLE OF INVENTION: Expression of Isoprenyl Protein Transferases
 NUMBER OF SEQUENCES: 36
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Lucas & Just
 STREET: 205 E. 42nd Street
 CITY: New York
 STATE: New York
 COUNTRY: USA
 ZIP: 10017

COMPUTER READABLE FORM:
 MEDIUM TYPE: Diskette, 3.50 inch,
 MEDIUM TYPE: 1.44 MB storage
 COMPUTER: IBM 486 Compatible
 OPERATING SYSTEM: MS-DOS 5.0
 SOFTWARE: WordPerfect 5.0
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/494,301A
 FILING DATE: 23-JUNE-1995
 CLASSIFICATION: 514
 PRIOR APPLICATION DATA:
 APPLICATION NUMBER: GB 9413035.8
 FILING DATE: 29-JUNE-1994
 INFORMATION FOR SEQ ID NO: 3:
 SEQUENCE CHARACTERISTICS:
 LENGTH: 12 base pairs
 TYPE: nucleotide
 STRANDEDNESS: single
 TOPOLOGY: linear
 ANTI-SENSE: Yes
 US-08-494-301A-3

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 Best Local Similarity 100.0%; Pred. No. 16;
 Matches 12; Conservative 0; Mismatches 0; Indels 0; Gaps 0;

QY 786 CTGCTACTCCTT 797
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 Db 12 CTGCTACTCCTT 1

RESULT 35

US-08-729-601A-71/c
 Sequence 71, Application US/08729601A
 Patent No. 6166302

GENERAL INFORMATION:
 APPLICANT: Merlo, Donald J.
 APPLICANT: Folkerts, Otto
 TITLE OF INVENTION: Modified Bacillus Thuringiensis Gene for
 TITLE OF INVENTION: Lepidopteran Control in Plants
 NUMBER OF SEQUENCES: 84
 CORRESPONDENCE ADDRESS:
 ADDRESSEE: Fitch, Sven, Tabin & Flannery
 STREET: 135 S. LaSalle St.
 CITY: Chicago
 STATE: IL
 COUNTRY: USA
 ZIP: 60603
 COMPUTER READABLE FORM:
 MEDIUM TYPE: Floppy disk
 COMPUTER: IBM PC compatible
 OPERATING SYSTEM: PC-DOS/MS-DOS
 SOFTWARE: Patent in Release #1.0, Version #1.25
 CURRENT APPLICATION DATA:
 APPLICATION NUMBER: US/08/729,601A
 FILING DATE:
 CLASSIFICATION: 800

OS Homo sapiens.
 XX WO200297114-A2.
 XX
 XX 05-DEC-2002.
 XX
 XX 29-MAY-2002; 2002WO-US016840.
 XX
 XX 29-MAY-2001; 2001US-0294140P.
 XX
 XX 06-JUN-2001; 2001US-0296249P.
 XX
 XX 10-SEP-2001; 2001US-0318471P.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.
 XX
 XX Mcswiggen J;
 XX
 XX WPI; 2003-140484/13.
 XX
 XX Novel short interfering RNA and enzymatic nucleic acid useful for
 PT treating cancer, modulates the expression of a nucleic acid encoding
 PT HER2, K-Ras, H-Ras, N-Ras, and human deficiency virus sequences.
 XX
 XX Claim 58; Page 130; 185pp; English.
 XX
 XX The invention relates to a novel short interfering RNA (siRNA) nucleic
 CC acid molecule or an enzymatic nucleic acid molecule, that modulates
 CC expression of a nucleic acid molecule encoding HER2, K-Ras, H-Ras, N-Ras,
 CC human immunodeficiency virus (HIV) or a component of HIV. The nucleic
 CC acid molecule of the invention has cytostatic, anti-HIV, and anti-
 CC rheumatic activity. The nucleic acid molecules are useful for reducing
 CC HER2, K-Ras, H-Ras, and HIV activity in a cell. The nucleic acids are
 CC also useful for treating breast, ovarian, colorectal, lung, prostate,
 CC bladder, or pancreatic cancer, and HIV infection, and AIDS. The sequences
 CC shown in ABZ59889 - ABZ62216, ABZ64544 - ABZ66531, ABZ66520 - ABZ66524,
 CC ABZ66530 - ABZ66585 represent substrate/target sequences for the human
 CC ribozymes of the invention
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 XX Sequence 17 BP; 0 A; 4 C; 8 G; 0 T; 5 U; 0 Other;
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 Best Local Similarity 64.3%; Pred. No. 67;
 Matches 9; Conservative 5; Mismatches 0; Indels 0; Gaps 0;
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 Db 3 GCCTGCTGCTGGT 16
 RESULT 67
 ADB42616/c
 ID ADB42616 standard; DNA; 17 BP.
 XX
 XX ADB42616;
 XX
 XX 18-DEC-2003 (revised)
 DT 04-DEC-2003 (first entry)
 XX
 XX Tumour suppression/reversion associated nucleotide #2939.
 DE
 XX cytostatic; antiviral; neuroprotective; nootropic; neuroleptic; ss;
 KW primer; probe; tumour suppression; tumour reversion; apoptosis;
 KW virus resistance; transgenic animals; Alzheimer's disease; schizophrenia;
 KW diagnosis.
 KW
 XX Homo sapiens.
 OS
 XX WO2003040369-A2.
 XX
 XX 15-MAY-2003.
 XX
 XX 17-SEP-2002; 2002WO-IB004219.
 XX
 XX 17-SEP-2001; 2001FR-00011981.

XX (MOLE-) MOLECULAR ENGINES LAB.
 XX
 XX Teherman A, Anson R, Tuijnder M;
 XX
 XX WPI; 2003-441574/41.
 XX
 XX New nucleic acid encoding human prostate membrane-specific antigen,
 PT useful e.g. for treatment of tumors and viral infection, also related
 PT polypeptide and antibodies.
 XX
 XX Disclosure; Page 375; 771pp; French.
 XX
 XX The invention relates to the isolation of 6327 nucleotide sequences,
 CC fragments of at least 15 consecutive nucleotides of these nucleotides, a
 CC sequence having at least 80% identity, after optimal alignment, with the
 CC nucleotides, a sequence that hybridizes under stringent conditions with
 CC the nucleotides, or the complement, or corresponding RNA, of the
 CC nucleotides. The nucleotides are used as probes or primers for detecting,
 CC identifying, quantifying and/or amplifying nucleic acids, as in vitro
 CC sense and antisense sequences, of nucleotides involved in tumour
 CC suppression or reversion, apoptosis and or viral resistance, to produce
 CC recombinant polypeptides, and to prepare transgenic animals, as
 CC experimental models. The nucleotides (also vectors containing them and
 CC cells containing the vectors), the encoded polypeptides and antibodies
 CC (Ab) against the polypeptide are useful for prevention and/or treatment
 CC of viral infections or diseases characterized by development of tumours
 CC or cell degeneration (e.g. Alzheimer's disease or schizophrenia).
 CC Analysis of the expression of the nucleotides can be used for diagnosis
 CC and/or prognosis of these diseases. The nucleotides and polypeptides can
 CC also be used to screen for their specific interactive molecules, and
 CC potentially useful for treating diseases associated with abnormal
 CC expression of the nucleotides.
 XX
 XX Sequence 17 BP; 7 A; 2 C; 5 G; 3 T; 0 U; 0 Other;
 SQ
 Query Match 1.3%; Score 14; DB 1; Length 17;
 Best Local Similarity 100.0%; Pred. No. 67;
 Matches 14; Conservative 0; Mismatches 0; Indels 0; Gaps 0;
 QY 821 CTTCCATATCTTGA 834
 |||:|:|:|:|:
 Db 16 CTTCCATATCTTGA 3
 RESULT 68
 AAX74847/c
 ID AAX74847 standard; RNA; 17 BP.
 XX
 XX AAX74847;
 AC
 XX 28-JUL-1999 (first entry)
 DT
 XX Mouse flt-1 VEGF receptor hammerhead ribozyme substrate #375.
 DE
 XX Vascular endothelial growth factor receptor; VEGF receptor; flt-1; flk-1;
 KW KDR; hammerhead ribozyme; hairpin ribozyme; cleavage;
 KW tumour angiogenesis; psoriasis; rheumatoid arthritis; ocular disease;
 KW fms-like tyrosine kinase 1; kinase insert domain containing receptor;
 KW foetal liver kinase 1; ss.
 KW
 XX Mus sp.
 OS
 XX WO9715662-A2
 XX
 XX 01-MAY-1997.
 PD
 XX 25-OCT-1996; 96WO-US017480.
 XX
 XX 26-OCT-1995; 95US-0005974P.
 XX
 XX 11-JAN-1996; 96US-00584040.
 XX
 XX (RIBO-) RIBOZYME PHARM INC.

PA (CHIR) CHIRON CORP.
XX Pavco P, Mcswiggen J, Stinchcomb D, Escobedo J;
XX WPI; 1997-259017/23.
XX
XX Nucleic acid molecule modulating VEGF receptor(s) gene expression or mRNA
XX stability - useful for treating e.g. tumour angiogenesis, psoriasis,
XX rheumatoid arthritis, etc., in a human patient.
XX
XX Claim 4; Page 166; 218pp; English.
XX
XX The present invention describes nucleic acid molecules which modulate the
XX synthesis, expression and/or stability of a mRNA encoding 1 or more
XX receptors of vascular endothelial growth factor (VEGF). A patient
XX (preferably human) having a condition associated with the level of the
XX fms-like tyrosine kinase 1 (flt-1), kinase insert domain containing
XX receptor (KDR) and/or foetal liver kinase 1 (flk-1) (e.g. tumour
XX angiogenesis, ocular diseases, psoriasis and rheumatoid arthritis) can be
XX treated by administering the nucleic acid molecule or the expression
XX vector to the patient. AA67275 to AA6752 represent specific examples
XX of nucleic acid molecules from the present invention
XX
XX Sequence 17 BP; 7 A; 0 C; 7 G; 0 T; 3 U; 0 Other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 88.2%; Pred. No. 70;
XX Matches 15; Conservative 0; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 427 CCGTTTCAGCATCTTC 443
XX DB 17 CCGTTTCAGCATCTTC 1
XX
XX RESULT 69
XX AAA18631
XX ID AAA18631 standard; RNA; 17 BP.
XX AC AAA18631;
XX
XX 19-JUN-2000 (first entry)
XX
XX Human TIE-2 substrate sequence SEQ ID NO:1857.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX

PS Claim 56; Page 107; 305pp; English.
XX
XX The present invention describes enzymatic nucleic acid molecules with RNA
XX cleaving activity, which specifically cleave RNA encoded by an aryl
XX hydrocarbon nuclear transporter (ARNT) gene, an integrin subunit beta 3
XX gene, an integrin alpha 6 subunit gene, or a Tie-2 gene. AAA16775 to
XX AAA17167 and AAA17561 to AAA17622 represent ribozyme sequences for ARNT,
XX and AAA17168 to AAA17560 and AAA17623 to AAA17684 represent their
XX corresponding target sequences; AAA17685 to AAA18385 and AAA19087 to
XX AAA19154 represent ribozyme sequences for Tie-2, and AAA18386 to AAA19086
XX and AAA19155 to AAA19222 represent their corresponding target sequences;
XX AAA19223 to AAA20361 and AAA21501 to AAA21595 represent ribozyme
XX sequences for integrin alpha 6 subunit, and AAA20362 to AAA21500 and
XX AAA21596 to AAA21688 represent their corresponding target sequences;
XX AAA21689 to AAA22475 and AAA23263 to AAA23342 represent ribozyme sequence
XX for integrin subunit beta 3, and AAA22476 to AAA23262, AAA23343 to
XX AAA23422 represent their corresponding target sequences. The ribozymes of
XX the invention are used for modulating the synthesis, expression and/or
XX stability of an mRNA encoding angiogenic factor, especially ARNT.
XX integrin subunit beta-3, integrin subunit alpha-6, or tie-2. They are
XX especially used to treat cancer, diabetic retinopathy, age related
XX macular degeneration (ARMD), inflammation, and arthritis, as well as
XX neovascular glaucoma, myopic degeneration, psoriasis, verruca vulgaris,
XX angiofibroma of tuberosus sclerosis, pot-wine stains, Sturge Weber
XX syndrome, Kippel-Trenaunay-Weber syndrome, Osler-Weber-Rendu syndrome,
XX and other syndromes and diseases related to the levels of ARNT, Tie-2,
XX integrin subunit alpha-6, or integrin subunit beta-3
XX
XX Sequence 17 BP; 9 A; 4 C; 2 G; 0 T; 2 U; 0 Other;
XX
XX Query Match 1.3%; Score 13.8; DB 1; Length 17;
XX Best Local Similarity 76.5%; Pred. No. 70;
XX Matches 13; Conservative 2; Mismatches 2; Indels 0; Gaps 0;
XX
XX QY 685 AATCAGATCCATGAAGC 901
XX DB 1 AAUCAAUCCAAAGAAGC 17
XX
XX RESULT 70
XX AAA20854/c
XX ID AAA20854 standard; RNA; 17 BP.
XX AC AAA20854;
XX
XX 19-JUN-2000 (first entry)
XX
XX Integrin alpha 6 subunit substrate sequence SEQ ID NO:4080.
XX
XX Human; aryl hydrocarbon nuclear transport; ARNT; TIE-2; angiogenesis;
XX integrin alpha 6 subunit; integrin subunit beta 3; hairpin ribozyme;
XX hammerhead ribozyme; angiogenic factor; cytosolic; antidiabetic;
XX ophthalmologic; antiinflammatory; antiarthritic; antipsoriatic; ARMD;
XX dermatological; RNA cleavage; cancer; diabetic retinopathy; arthritis;
XX age related macular degeneration; inflammation; neovascular glaucoma;
XX myopic degeneration; psoriasis; verruca vulgaris; angiofibroma;
XX Kippel-Trenaunay-Weber syndrome; Osler-Weber-Rendu syndrome; ss.
XX
XX Homo sapiens.
XX
XX WO9950403-A2.
XX
XX 07-OCT-1999.
XX
XX 24-MAR-1999; 99WO-US006507.
XX
XX 27-MAR-1998; 98US-0079678P.
XX
XX (RIBO-) RIBOZYME PHARM INC.
XX
XX Pavco PA, Roberts E, Jarvis T, Coeshott C, Mcswiggen JA;
XX WPI; 1999-591315/50.
XX
XX Novel ribozymes for modulating the synthesis, expression and/or stability
XX of an mRNA encoding an angiogenic factors.
XX

SCORE OVER LENGTH SEARCHES

Attached is a score over length search. This search was developed to overcome limitations in most standard search systems which favor large sequences with high scoring, but lesser overall identity over smaller sequences with higher overall identity. This search is especially useful for relatively small nucleic acid or polypeptide target sequences (antisense, fragments, probes, primers, RNAi, epitopes, haptens, etc.) claimed functionally via a form of hybridization and/or identity language and having defined upper and lower polynucleotide and or polypeptide length limits.

The score over length search is performed by first running the query sequence using examiner-specified identity and polynucleotide or protein length limit parameters, and saving 65,000 hits and 0 alignments from each desired database. The resulting output is reformatted using a Microsoft Word macro and is imported into Excel. The summary table data are then sorted by the ratio of score of each hit sequence divided by its length and the accession numbers for all hits below the examiner's desired score over length parameters are deleted. The remaining accession numbers are used to pull the corresponding sequences from the databases into subdatabases enriched for good hits and the query sequence is re-run against these subdatabases to yield the final results.

The score over length cutoff for this search is 80%.

Examiner Please Note: This cover sheet should be included when submitting results to be scanned.